

REMARKS

The above amendments have been made in order to incorporate the amendments made in parent Application Serial No. 09/463,048 as well as add new claims 18-22. Also, in order to comply with 37 C.F.R. 1.821 through 1.825, Applicant respectfully submits they are in compliance with such provisions by way of the attached herein-submitted substitute Sequence Listing and the herein-presented amendments to the specification and Figure 6.

Sequence Listing

The substitute Sequence Listing is herein submitted to comply with the requirements for an application containing a nucleotide and/or amino acid sequence and in particular sets forth the primers identified in Figures 1 and 4 as SEQ ID NOS: 7-20.

Hereto is an attached substitute paper copy of the Sequence Listing. The computer readable format was filed in parent Application Serial No. 09/463,048. The paper copy and computer readable copy of the substitute Sequence Listing are the same. The substitute Sequence Listing does not include new matter.

Specification

The specification is amended to insert sequence identifiers in the figure legends for all sequences identified in the substitute Sequence Listing.

Figures

The attached amended formal drawings of Figures 6A and 6B are amended to add the stop codon "taa" to the end of the upper sequence of Figure 6B. Applicant respectfully submits that the added "taa" stop codon is not new matter, but rather, it is matter already disclosed in the

originally filed specification. Applicant submits that it is obvious from reading the specification and comparing sequences that Figures 6A and 6B set forth the alignment of SEQ ID NO:1 and SEQ ID NO:2.

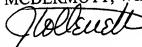
The brief description of Figure 6 states that Figure 6 (now Figures 6A and 6B) shows the "Alignment of the nucleotide sequences encompassing the protein open reading frames of the *X. nematophilus* strain A24tox4 gene and the *P. luminescens* strain V16/1 *PIV16tox1* gene using the Gap program of the GCG computer software package. The *X. nematophilus* sequence is the upper line and the *P. luminescens* sequence is the lower line." The lower sequence of Figure 6 as originally filed (now Figures 6A and 6B), identified as the nucleotide sequence encompassing the protein open reading frame of *P. luminescens* strain V16/1 *PIV16tox1* gene, is identical to SEQ ID NO:2. Thus, the SEQ ID NO:2 and the lower sequence of Figures 6A and 6B are the protein open reading frame of *P. luminescens* strain V16/1 *PIV16tox1* gene.

With respect to the upper sequence of Figures 6A continuing onto 6B, which corresponds to the *X. nematophilus* strain A24tox4 gene, this sequence as originally filed is 1104 nucleotides in length. The sequence length of SEQ ID NO:1 is 1107 nucleotides. A nucleotide to nucleotide comparison of SEQ ID NO:1 and the upper sequence set out in originally filed Figure 6 (now Figures 6A and 6B) reveals that the two sequences are identical except that the upper sequence in Figures 6B omits the "taa" stop codon at the end of the sequence. The herein presented Figure 6B replaces the "..." of the upper sequence with the "taa" stop codon, thereby making the total nucleotide sequence length equal to 1107 nucleotides as disclosed in SEQ ID NO:1.

Entry of this Preliminary Amendment is respectfully requested.

Respectfully submitted,

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